

OIPF

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/854,300

DATE: 06/05/2001

TIME: 08:24:22

Input Set : A:\Seqlist.txt

Output Set: C:\CRF3\06052001\I854300.raw

ENTERED

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4 <110> APPLICANT: Ford, Gregory
5      Bloom, Debra
6      Fathman, C. Garrison
8 <120> TITLE OF INVENTION: Anergy Associated Genes
11 <130> FILE REFERENCE: STAN177
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/854,300
C--> 14 <141> CURRENT FILING DATE: 2001-05-15
16 <150> PRIOR APPLICATION NUMBER: 60/203,513
17 <151> PRIOR FILING DATE: 2000-05-11
19 <160> NUMBER OF SEQ ID NOS: 8
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 239
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus musculus
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30 aactgtcaaa tcaatttcta gctctaaat ctgtctactt ccactccaca agtcacata      120
31 agagagaagc tgatggaaat ttttgagtc ctttcattag ataattgaca tactcagttt      180
32 ccttttgaac acagtccttg gtaataggaa tcatacagaa atcttttatt tctggaaaa      239
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 260
36 <212> TYPE: DNA
37 <213> ORGANISM: Mus musculus
39 <400> SEQUENCE: 2
40 ggattttggc tccggggcat cctggattta gaaaacggac agcacacagt acagtggat      60
41 aaacttttta ttatcagttc aaaatcagtt tgtgttcag aagaaagatt gctaattgat      120
42 gatgggaagt gtttgccat gcttgcttgt tggcagttaa gacaaatgta acacacacac      180
43 acacacacac acacacacac acacatgaga tgagtcactg ccttctatgg ccttctatgg      240
44 tgtacgacag tttagatgc      260
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 500
48 <212> TYPE: DNA
49 <213> ORGANISM: Mus musculus
51 <400> SEQUENCE: 3
52 cccagcaaga cctcagccat gagacttctc ctctgactt tcttgggagt ctgtgcctc      60
53 acccatggg ttgtggaagg tgtggggact gaagtcctag aagagagtag ctgtgtgaac      120
54 ttacaaaccc agcggctgcc agttcaaaaa atcaagacct atatcatctg ggagggggcc      180
55 atgagagctg taatttttgt caccaaacga ggactaaaaa tttgtgctga tccagaaccc      240
56 aaatgggtga aagcagcgat caagactgtg gatggcaggg ccagtaccag aaagaacatg      300
57 gctgaaactg tccacacagg agcccagagg tccaccagca cagcagtaac cctgactggg      360
58 taacagctc caggacaatg tttcctcact cgtaaagcag ctcatctcag ttcccaaacc      420
59 cattgcacaa atacttattt ttatttttaa cgacattcac attcatttca aatgttataa      480
60 gtaataaata ttattattg      500
62 <210> SEQ ID NO: 4
63 <211> LENGTH: 264
64 <212> TYPE: DNA

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65 <213> ORGANISM: Mus musculus
67 <400> SEQUENCE: 4
68 agccgaatta tacaatttca cacaggaatg gtagtctgaa ggtcctgatt tttcagtgtt      60
69 tcaaactaat gcagaaagaa aaaggaaaat gtgtgttgta ttgtcttcac tactgagtct      120
70 tttctttggg aaccatcact gttgagaggt gggggaaaac ctgaatgtaa aaagcattta      180
71 tttgtcaata aactgccttt tgtaaaaaaa agccctatag tgagtcgtat tacaagccga      240
72 ttctgcgaaa ttccatcaca ctaa                                264
74 <210> SEQ ID NO: 5
75 <211> LENGTH: 2145
76 <212> TYPE: DNA
77 <213> ORGANISM: Mus musculus
79 <220> FEATURE:
80 <221> NAME/KEY: CDS
81 <222> LOCATION: (358)...(1641)
83 <400> SEQUENCE: 5
84 caagcgatta agttgggttaa cgccaggttt tcccgatcac gacggttgta aaacgacggg      60
85 ccagtaattg taatacgacc tcactatagg gcgaattggg tacacttacc tggtagccca      120
86 cccgggtgga aaatcgatgg gcccgcgggc gctctagaag tactctcgag aagctttttg      180
87 aattcggcac gagecgttgc ttgcaggagc tgcgtctgca gtagcctggc cgctgacgct      240
88 gcgtgccggc tggcagggca gectgcgacc tcgctggccc cgcgccgct gctagccgcc      300
89 ggctccccac ctggttcgca cctagtccca gcccggtcg cctgccgagt gcgcgcc atg      360
90                                     Met
91                                     1
93 ggg ccg ccg ccc ggg atc ggg gtc tac tgc cgc ggc ggc tgc gga gct      408
94 Gly Pro Pro Pro Gly Ile Gly Val Tyr Cys Arg Gly Gly Cys Gly Ala
95           5                10                15
97 gcc ccg cta ctg gct tgg tgc ttc ctt ctg gct ctg agt ccg cac gcg      456
98 Ala Arg Leu Leu Ala Trp Cys Phe Leu Leu Ala Leu Ser Pro His Ala
99           20                25                30
101 ccc ggt tcc ccg gga gcc gaa gcc gtg tgg act gcg tac ctc aac gtg      504
102 Pro Gly Ser Arg Gly Ala Glu Ala Val Trp Thr Ala Tyr Leu Asn Val
103           35                40                45
105 tcc tgg ccg gtt ccg cac acc gga gtg acc gca ccg tgt gga gct gag      552
106 Ser Trp Arg Val Pro His Thr Gly Val Thr Ala Arg Cys Gly Ala Glu
107           50                55                60                65
109 cga gag ggc gtg tac ggc cag gac tcg ccg ctg aag ccc gtc tcc ggg      600
110 Arg Glu Gly Val Tyr Gly Gln Asp Ser Pro Leu Lys Pro Val Ser Gly
111           70                75                80
113 gtc ctg gta ccg ccc gac ggg ccc ggg gcg ctc aac gcc tgt aac ccg      648
114 Val Leu Val Pro Pro Asp Gly Pro Gly Ala Leu Asn Ala Cys Asn Pro
115           85                90                95
117 cac acc aat ttc acg gtg ccc acg gtt tgg ggg agc acg gtg caa gta      696
118 His Thr Asn Phe Thr Val Pro Thr Val Trp Gly Ser Thr Val Gln Val
119           100               105               110
121 tct tgg ttg gcc ctc atc caa cgc ggt gga ggc tgc acc ttc gcg gac      744
122 Ser Trp Leu Ala Leu Ile Gln Arg Gly Gly Gly Cys Thr Phe Ala Asp
123           115               120               125
125 aag atc cat ctg gct tca gag aga ggg gct tct gga gcg gtc atc ttt      792
126 Lys Ile His Leu Ala Ser Glu Arg Gly Ala Ser Gly Ala Val Ile Phe

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127	130				135					140				145			
129	aac	ttc	cct	ggg	acc	cgc	aat	gag	gtc	atc	ccc	atg	tct	cac	ccg	ggt	840
130	Asn	Phe	Pro	Gly	Thr	Arg	Asn	Glu	Val	Ile	Pro	Met	Ser	His	Pro	Gly	
131					150					155				160			
133	gct	ggg	gac	att	gtt	gca	atc	atg	att	ggc	aat	ctg	aaa	gga	aca	aaa	888
134	Ala	Gly	Asp	Ile	Val	Ala	Ile	Met	Ile	Gly	Asn	Leu	Lys	Gly	Thr	Lys	
135				165					170					175			
137	att	ctg	cag	tct	att	caa	aga	ggc	atc	caa	gtc	aca	atg	gtc	atc	gaa	936
138	Ile	Leu	Gln	Ser	Ile	Gln	Arg	Gly	Ile	Gln	Val	Thr	Met	Val	Ile	Glu	
139			180					185					190				
141	gta	ggg	aaa	aaa	cat	ggc	cct	tgg	gtg	aat	cat	tat	tca	att	ttc	ttc	984
142	Val	Gly	Lys	Lys	His	Gly	Pro	Trp	Val	Asn	His	Tyr	Ser	Ile	Phe	Phe	
143		195				200				205							
145	gtt	tct	gtg	tcc	ttt	ttc	ata	att	acg	gca	gca	acc	gtg	ggc	tat	ttc	1032
146	Val	Ser	Val	Ser	Phe	Phe	Ile	Ile	Thr	Ala	Ala	Thr	Val	Gly	Tyr	Phe	
147	210				215					220					225		
149	atc	ttt	tat	tct	gct	cga	aga	tta	cga	aat	gca	aga	gct	caa	agc	agg	1080
150	Ile	Phe	Tyr	Ser	Ala	Arg	Arg	Leu	Arg	Asn	Ala	Arg	Ala	Gln	Ser	Arg	
151				230					235					240			
153	aag	cag	agg	cag	tta	aag	gca	gat	gct	aaa	aaa	gct	att	gga	aag	ctt	1128
154	Lys	Gln	Arg	Gln	Leu	Lys	Ala	Asp	Ala	Lys	Lys	Ala	Ile	Gly	Lys	Leu	
155			245				250					255					
157	cag	ctg	cgc	acc	ttg	aaa	caa	gga	gac	aag	gaa	att	ggc	cct	gat	gga	1176
158	Gln	Leu	Arg	Thr	Leu	Lys	Gln	Gly	Asp	Lys	Glu	Ile	Gly	Pro	Asp	Gly	
159			260				265					270					
161	gat	agc	tgt	gct	gtg	tgc	att	gag	ctc	tat	aag	cca	aat	gat	ttg	gtg	1224
162	Asp	Ser	Cys	Ala	Val	Cys	Ile	Glu	Leu	Tyr	Lys	Pro	Asn	Asp	Leu	Val	
163		275				280					285						
165	cgc	atc	cta	acc	tgc	aat	cat	att	ttc	cat	aag	aca	tgt	gtg	gac	ccg	1272
166	Arg	Ile	Leu	Thr	Cys	Asn	His	Ile	Phe	His	Lys	Thr	Cys	Val	Asp	Pro	
167	290				295					300					305		
169	tgg	ctt	tta	gaa	cac	agg	act	tgc	ccc	atg	tgc	aag	tgt	gac	att	ctc	1320
170	Trp	Leu	Leu	Glu	His	Arg	Thr	Cys	Pro	Met	Cys	Lys	Cys	Asp	Ile	Leu	
171			310						315					320			
173	aaa	gct	ctg	gga	att	gag	gtg	gat	gtt	gaa	gat	gga	tca	gtg	tct	tta	1368
174	Lys	Ala	Leu	Gly	Ile	Glu	Val	Asp	Val	Glu	Asp	Gly	Ser	Val	Ser	Leu	
175			325				330					335					
177	caa	gtt	cct	gtt	tct	aat	gaa	gca	tct	aat	act	gcc	tct	ccc	cat	gaa	1416
178	Gln	Val	Pro	Val	Ser	Asn	Glu	Ala	Ser	Asn	Thr	Ala	Ser	Pro	His	Glu	
179			340				345					350					
181	gag	gac	agt	cgc	agt	gag	act	gca	tca	tct	gga	tat	gct	tca	gta	caa	1464
182	Glu	Asp	Ser	Arg	Ser	Glu	Thr	Ala	Ser	Ser	Gly	Tyr	Ala	Ser	Val	Gln	
183		355				360					365						
185	gga	gca	gat	gag	cca	cct	ctg	gag	gaa	cat	gcg	cag	tca	gca	aat	gaa	1512
186	Gly	Ala	Asp	Glu	Pro	Leu	Glu	Glu	His	Ala	Gln	Ser	Ala	Asn	Glu		
187	370				375					380				385			
189	aat	cta	cag	ctg	gta	aac	cat	gaa	gca	aat	tct	gtg	gcc	gtg	gat	gtt	1560
190	Asn	Leu	Gln	Leu	Val	Asn	His	Glu	Ala	Asn	Ser	Val	Ala	Val	Asp	Val	
191				390					395					400			

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193 gtt ccc cat gtt gac aac cca acc ttt gaa gaa gat gaa act cct gat      1608
194 Val Pro His Val Asp Asn Pro Thr Phe Glu Glu Asp Glu Thr Pro Asp
195              405              410              415
197 caa gag gca gct gtt cgg gag att aaa tct taa aaatctgtgt caatagaaaa      1661
198 Gln Glu Ala Ala Val Arg Glu Ile Lys Ser *
199              420              425
201 cttgaaccgt tagttaacaa caggactgcc aatcagggcc tagtttacta tgaatgaact      1721
202 gggtaaacgt aaaacaagaa tgatactgaa agtgctgagg taacttatat tatactatag      1781
203 ttaaatggct taacataattt accccagtag cgttttccac aaactcacca taacgttttt      1841
204 cataggcaag tttcctcttg gtgatatgta tagcaacatt ttaacattc agaaccgtct      1901
205 atgagtagtc aggtttttca tttacaacaa ctttggtata aaaaaatatg ttgctttaaa      1961
206 agtgtggagt agctgtaatc actttgtttt atgatagtat cataattaaa caatactact      2021
207 actttagctt gggctctgtg tgctcggtt tgtctccagg tgcttatatt gatctggaat      2081
208 ttgttttaaaa aaactcgtgc cgaattcttt ggatccacta gtgtcgacct gcaggcgcg      2141
209 gaggc                                          2145
211 <210> SEQ ID NO: 6
212 <211> LENGTH: 427
213 <212> TYPE: PRT
214 <213> ORGANISM: Mus musculus
216 <400> SEQUENCE: 6
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218 1              5              10              15
219 Ala Ala Arg Leu Leu Ala Trp Cys Phe Leu Leu Ala Leu Ser Pro His
220              20              25              30
221 Ala Pro Gly Ser Arg Gly Ala Glu Ala Val Trp Thr Ala Tyr Leu Asn
222              35              40              45
223 Val Ser Trp Arg Val Pro His Thr Gly Val Thr Ala Arg Cys Gly Ala
224              50              55              60
225 Glu Arg Glu Gly Val Tyr Gly Gln Asp Ser Pro Leu Lys Pro Val Ser
226 65              70              75              80
227 Gly Val Leu Val Pro Pro Asp Gly Pro Gly Ala Leu Asn Ala Cys Asn
228              85              90              95
229 Pro His Thr Asn Phe Thr Val Pro Thr Val Trp Gly Ser Thr Val Gln
230              100             105             110
231 Val Ser Trp Leu Ala Leu Ile Gln Arg Gly Gly Gly Cys Thr Phe Ala
232              115             120             125
233 Asp Lys Ile His Leu Ala Ser Glu Arg Gly Ala Ser Gly Ala Val Ile
234              130             135             140
235 Phe Asn Phe Pro Gly Thr Arg Asn Glu Val Ile Pro Met Ser His Pro
236 145             150             155             160
237 Gly Ala Gly Asp Ile Val Ala Ile Met Ile Gly Asn Leu Lys Gly Thr
238              165             170             175
239 Lys Ile Leu Gln Ser Ile Gln Arg Gly Ile Gln Val Thr Met Val Ile
240              180             185             190
241 Glu Val Gly Lys Lys His Gly Pro Trp Val Asn His Tyr Ser Ile Phe
242              195             200             205
243 Phe Val Ser Val Ser Phe Phe Ile Ile Thr Ala Ala Thr Val Gly Tyr
244              210             215             220
245 Phe Ile Phe Tyr Ser Ala Arg Arg Leu Arg Asn Ala Arg Ala Gln Ser

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246 225          230          235          240
247 Arg Lys Gln Arg Gln Leu Lys Ala Asp Ala Lys Lys Ala Ile Gly Lys
248          245          250          255
249 Leu Gln Leu Arg Thr Leu Lys Gln Gly Asp Lys Glu Ile Gly Pro Asp
250          260          265          270
251 Gly Asp Ser Cys Ala Val Cys Ile Glu Leu Tyr Lys Pro Asn Asp Leu
252          275          280          285
253 Val Arg Ile Leu Thr Cys Asn His Ile Phe His Lys Thr Cys Val Asp
254          290          295          300
255 Pro Trp Leu Leu Glu His Arg Thr Cys Pro Met Cys Lys Cys Asp Ile
256 305          310          315          320
257 Leu Lys Ala Leu Gly Ile Glu Val Asp Val Glu Asp Gly Ser Val Ser
258          325          330          335
259 Leu Gln Val Pro Val Ser Asn Glu Ala Ser Asn Thr Ala Ser Pro His
260          340          345          350
261 Glu Glu Asp Ser Arg Ser Glu Thr Ala Ser Ser Gly Tyr Ala Ser Val
262          355          360          365
263 Gln Gly Ala Asp Glu Pro Pro Leu Glu Glu His Ala Gln Ser Ala Asn
264          370          375          380
265 Glu Asn Leu Gln Leu Val Asn His Glu Ala Asn Ser Val Ala Val Asp
266 385          390          395          400
267 Val Val Pro His Val Asp Asn Pro Thr Phe Glu Glu Asp Glu Thr Pro
268          405          410          415
269 Asp Gln Glu Ala Ala Val Arg Glu Ile Lys Ser
270          420          425
272 <210> SEQ ID NO: 7
273 <211> LENGTH: 1774
274 <212> TYPE: DNA
275 <213> ORGANISM: Homo sapiens
277 <220> FEATURE:
278 <221> NAME/KEY: CDS
279 <222> LOCATION: (263)...(1547)
281 <221> NAME/KEY: misc_feature
282 <222> LOCATION: (1)...(1774)
283 <223> OTHER INFORMATION: n = A,T,C or G
285 <400> SEQUENCE: 7
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287 aattcggcac gagccgagga gctgcacatg cggaacctg tgtgctgacg ctacgtgcct      120
288 cctggctccg acgtagctcg cagctcccca gtctcactcc attccttccc cacctggcgc      180
289 gcacctgctc aagaccaggg tctgccaag cgctaggagg gcgcgtgccg ggggcgctag      240
290 ggaactgcgg agcgcgcgcg cc atg ggg ccg ccg cct ggg gcc ggg gtc tcc      292
291          Met Gly Pro Pro Pro Gly Ala Gly Val Ser
292          1          5          10
294 tgc cgc ggt ggc tgc ggc ttt tcc aga ttg ctg gca tgg tgc ttc ctg      340
295 Cys Arg Gly Gly Cys Gly Phe Ser Arg Leu Leu Ala Trp Cys Phe Leu
296          15          20          25
298 ctg gcc ctg agt ccg cag gca ccc ggt tcc cgg ggg gct gaa gca gtg      388
299 Leu Ala Leu Ser Pro Gln Ala Pro Gly Ser Arg Gly Ala Glu Ala Val
300          30          35          40

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7